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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/441,055A

DATE: 02/28/2002
TIME: 13:18:42

Input Set : A:\001010570.txt
Output Set: N:\CRF3\02282002\I441055A.raw

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3 <110> APPLICANT: USUDA, YOSHIHIRO
4      KURAHASHI, OSAMU
6 <120> TITLE OF INVENTION: METHOD FOR PRODUCING L-METHIONINE BY FERMENTATION
8 <130> FILE REFERENCE: 0010-1057-0
10 <140> CURRENT APPLICATION NUMBER: 09/441,055A
11 <141> CURRENT FILING DATE: 1999-11-16
13 <150> PRIOR APPLICATION NUMBER: JP 10-326717
14 <151> PRIOR FILING DATE: 1998-11-17
16 <160> NUMBER OF SEQ ID NOS: 29
18 <170> SOFTWARE: PatentIn version 3.1
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23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Synthetic DNA
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127 cacagacgca tgccc 75
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183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
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194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
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Input Set : A:\001010570.txt
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217 <211> LENGTH: 1155
 218 <212> TYPE: DNA
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 221 <220> FEATURE:
 222 <221> NAME/KEY: CDS
 223 <222> LOCATION: (1)..(1152)
 224 <223> OTHER INFORMATION:
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230 1 5 10 15	
232 gac aaa att gct gac caa att tct gat gcc gtt tta gac gcg atc ctc	96
233 Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu	
234 20 25 30	
236 gaa cag gat ccg aaa gca cgc gtt gct tgc gaa acc tac gta aaa acc	144
237 Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr	
238 35 40 45	
240 ggc atg gtt tta gtc ggc gaa atc acc acc agc gcc tgg gta gac	192
241 Gly Met Val Leu Val Gly Glu Ile Thr Thr Ser Ala Trp Val Asp	
242 50 55 60	
244 atc gaa gag atc acc cgt aac acc gtt cgc gaa att ggc tat gtg cat	240
245 Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His	
246 65 70 75 80	
248 tcc gac atg ggc ttt gac gct aac tcc tgt gcg gtt ctg agc gct atc	288
249 Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile	
250 85 90 95	
252 ggc aaa cag tct cct gac atc aac cag ggc gtt gac cgt gcc gat ccg	336
253 Gly Lys Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Ala Asp Pro	
254 100 105 110	
256 ctg gaa cag ggc gcg ggt gac cag ggt ctg atg ttt ggc tac gca act	384
257 Leu Glu Gln Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr	
258 115 120 125	
260 aat gaa acc gac gtg ctg atg cca gca cct atc acc tat gca cac cgt	432
261 Asn Glu Thr Asp Val Leu Met Pro Ala Pro Ile Thr Tyr Ala His Arg	
262 130 135 140	
264 ctg gta cag cgt cag gct gaa gtg cgt aaa aac ggc act ctg ccg tgg	480
265 Leu Val Gln Arg Gln Ala Glu Val Arg Lys Asn Gly Thr Leu Pro Trp	
266 145 150 155 160	
268 ctg cgc ccg gac gcg aaa agc cag gtg act ttt cag tat gac gac ggc	528
269 Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Phe Gln Tyr Asp Asp Gly	
270 165 170 175	
272 aaa atc gtt ggt atc gat gct gtc gtg ctt tcc act cag cac tct gaa	576
273 Lys Ile Val Gly Ile Asp Ala Val Val Leu Ser Thr Gln His Ser Glu	
274 180 185 190	
276 gag atc gac cag aaa tcg ctg caa gaa gcg gta atg gaa gag atc atc	624
277 Glu Ile Asp Gln Lys Ser Leu Gln Glu Ala Val Met Glu Glu Ile Ile	
278 195 200 205	
280 aag cca att ctg ccc gct gaa tgg ctg act tct gcc acc aaa ttc ttc	672
281 Lys Pro Ile Leu Pro Ala Glu Trp Leu Thr Ser Ala Thr Lys Phe Phe	

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282	210	215	220	
284	atc aac ccg acc ggt cgt ttc gtt atc ggt ggc cca atg ggt gac tgc			720
285	Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly Pro Met Gly Asp Cys			
286	225	230	235	240
288	ggt ctg act ggt cgt aaa att atc gtt gat acc tac ggc ggc atg gcg			768
289	Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala			
290	245	250	255	
292	cgt cac ggt ggc ggt gca ttc tct ggt aaa gat cca tca aaa gtg gac			816
293	Arg His Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp			
294	260	265	270	
296	cgt tcc gca gcc tac gca gca cgt tat gtc gcg aaa aac atc gtt gct			864
297	Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Ile Val Ala			
298	275	280	285	
300	gct ggc ctg gcc gat cgt tgt gaa att cag gtt tcc tac gca atc ggc			912
301	Ala Gly Leu Ala Asp Arg Cys Glu Ile Gln Val Ser Tyr Ala Ile Gly			
302	290	295	300	
304	gtg gct gaa ccg acc tcc atc atg gta gaa act ttc ggt act gag aaa			960
305	Val Ala Glu Pro Thr Ser Ile Met Val Glu Thr Phe Gly Thr Glu Lys			
306	305	310	315	320
308	gtg cct tct gaa caa ctg acc ctg ctg gta cgt gag ttc ttc gac ctg			1008
309	Val Pro Ser Glu Gln Leu Thr Leu Leu Val Arg Glu Phe Phe Asp Leu			
310	325	330	335	
312	cgc cca tac ggt ctg att cag atg ctg gat ctg ctg cac ccg atc tac			1056
313	Arg Pro Tyr Gly Leu Ile Gln Met Leu Asp Leu Leu His Pro Ile Tyr			
314	340	345	350	
316	aaa gaa acc gca gca tac ggt cac ttt ggt cgt gaa cat ttc ccg tgg			1104
317	Lys Glu Thr Ala Ala Tyr Gly His Phe Gly Arg Glu His Phe Pro Trp			
318	355	360	365	
320	gaa aaa acc gac aaa gcg cag ctg ctg cgc gat gct gcc ggt ctg aag			1152
321	Glu Lys Thr Asp Lys Ala Gln Leu Leu Arg Asp Ala Ala Gly Leu Lys			
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328	<211> LENGTH: 384			
329	<212> TYPE: PRT			
330	<213> ORGANISM: Escherichia coli			
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339	20	25	30	
342	Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr			
343	35	40	45	
346	Gly Met Val Leu Val Gly Gly Glu Ile Thr Thr Ser Ala Trp Val Asp			
347	50	55	60	
350	Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His			
351	65	70	75	80
354	Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile			
355	85	90	95	

VERIFICATION SUMMARY
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